

Amendments to the Claims

This Listing of Claims will replace all prior listings, and versions, in this application.

Listing of Claims

1-35. (Canceled)

36. (Currently Amended) A method for identifying a molecular interaction network representation for a set of interacting molecules within a known biological system, wherein each of said interacting molecules have one or more conserved features, the method comprising using a computer to execute instructions in a computer readable medium to perform the steps of:

- (a) determining attraction probabilities between pairs of molecules of the set of interacting molecules based on known molecular interaction data wherein said determining attraction probabilities comprises quantifying the occurrence frequency of said conserved features of said pair of molecules immediately upstream or downstream of each other within known biological system networks;
- (b) determining an edge probability $P(E)$, which is the probability of a single network with a particular edge set, for each possible molecular interaction network of the set of interacting molecules, based on the determined attraction probabilities of each pair of interacting molecules within said each possible molecular interaction network;
- (c) determining a network topology probability $P(\text{topology})$, which is defined as the probability that the network has a particular distribution of edges going into and out of each vertex of the network, for said each possible molecular interaction network based on the network topology of said network, said topology probability being a product of an incoming edge distribution probability which is the probability the network has a particular distribution of edges going into each vertex of the network and an outgoing edge distribution probability, which is the probability the network has a particular distribution of edges going out of each vertex of the network, within said each possible molecular interaction network;

- (d) determining a network probability of said each possible molecular interaction network as a product of said edge probability $P(E)$ and said topology probability $P(\text{topology})$;
- (e) determining a posterior probability of said each possible molecular interaction network using the following equation ~~equation 10~~;

$$P(\text{network}_i | \text{data}) = \frac{P(\text{data} | \text{network}_i)P(\text{network}_i)}{\sum_{\text{all networks}} P(\text{data} | \text{network}_j)P(\text{network}_j)}.$$

- (f) identifying the possible molecular interaction network having the highest posterior probability as said molecular interaction network representation for the set of interacting molecules; and
- (g) providing said molecular interaction network representation for the set of interacting molecules to a user or further processor.

37. (Previously presented) The method of claim 36, wherein said molecule is a protein and said conserved features are protein domain or motif.

38. (Currently Amended) A method for identifying a molecular interaction of a molecule within a biological network of interacting molecules, said interacting molecules each having one or more conserved features, the method comprising using a computer to execute instructions in a computer readable medium to perform the steps of:

- (a) identifying a conserved feature of said molecule;
- (b) determining probabilities of attraction between the conserved features of said molecule and other interacting molecules based on known molecular interaction data of the biological network;
- (c) determining probabilities of molecular interactions of said molecule with each of the other interacting molecules based on the probabilities of attraction;
- (d) identifying the molecular interaction of said molecule with one of the other interacting molecules, corresponding to the highest of the determined probabilities of molecular interactions; and
- (e) providing the identification of the molecular interaction corresponding to the highest of the determined molecular interaction probabilities to a user or further processor.

39. (Currently Amended) The method of claim 38, wherein said attraction probabilities of said features are determined by using either equation 6 or 14.

$$p(d_m, d_n) = \frac{1}{2} \left(1 + \frac{k_{mn}}{k_m k_n + \Psi} \right),$$

or

$$\hat{p}(d_i, d_j) = \frac{n_{ij}^+ + \Psi / 2}{n_{ij}^+ + m_{ij}^- + \Psi}$$

40. (Currently Amended) The method of claim 38, wherein said attraction probabilities of said features are determined by using the following equation: equation 14.

$$\hat{p}(d_i, d_j) = \frac{n_{ij}^+ + \Psi / 2}{n_{ij}^+ + m_{ij}^- + \Psi}$$

41. (Currently Amended) The method of claim 38, wherein said molecular probability of the molecular interaction between said two molecules is identified by using: equations 5 or 17.

$$p_{ij} = \sum_{d_m \in v_i} \sum_{d_n \in v_j} \frac{p(d_m, d_n)}{|v_i| |v_j|}.$$

or

$$\hat{p}_{ij} = \frac{\sum_{d_k \in v_i} \sum_{d_l \in v_j} \hat{p}(d_k, d_l) (f_k f_l)^{-1}}{\sum_{d_x \in v_i} \sum_{d_y \in v_j} (f_x f_y)^{-1}}$$

42. (Currently Amended) The method of claim 38, wherein said likelihood of molecular interactions between said interacting molecules is determined by using the following equation: equations 17.

$$\hat{p}_{ij} = \frac{\sum_{d_k \in v_i} \sum_{d_l \in v_j} \hat{p}(d_k, d_l) (f_k f_l)^{-1}}{\sum_{d_x \in v_i} \sum_{d_y \in v_j} (f_x f_y)^{-1}}$$

43. (Previously Presented) The method of claim 38, wherein said molecules are protein, and said conserved features are protein domain or motif.

44. (Previously Presented) A screening method for testing whether a compound is capable of modifying the interaction between at least two molecules in a biology network, the method comprising:

identifying an interaction between said at least two molecules using the method of claim 38;

introducing said compound in the biology network, said compound contacting said at least two molecules; and

comparing the identified interaction of the molecules in the presence of said compound with the identified interaction in the absence of said compound;

wherein a difference in the identified interaction of the molecules in the presence of said compound as compared to the interaction in the absence of a test compound indicates identification of said compound as a compound capable of modifying the interaction between molecules.

45. (Previously Presented) The screening method of claim 44, wherein said molecules are proteins.